This study investigates the spread of infectious diseases by simulating the Susceptible-Infected-Recovered (SIR) model

Introduction The dynamics of infectious diseases depend not only on pathogen properties but also on the structure of co

behavior. For reproducibility, all code for network construction and experiment setup is available in the Appendix. [ht] [wid

Results Qualitative and quantitative analysis of the simulation output reveals several core phenomena. The infected po

homogeneous contact structure can grossly underestimate the role of superspreading and network-driven persistence. Strate

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*Appendices *A. Network and Model Construction Code Code used to generate the network, set parameters, and perfo

```
# network_construction.py
import networkx as nx
from scipy import sparse
n = 1000
m = 4
G = nx.barabasi_albert_graph(n, m, seed=42)
sparse.save_npz('network.npz', nx.to_scipy_sparse_array(G))

# parameter_setting.py
R0 = 2.5
gamma = 1/7
... (see above)
```

*B. Additional Plots [ht] [width=0.48]results-11-review.png Detailed time-series for all SIR populations.